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ST.25 numeric identifier	Transformation performed by the tool
160	Discard element 160 (number of SEQ ID numbers)
170	Discard element 170 (Software used)
210	Element 210: set sequence identifier (SEQ ID)
n.a.	Set sequence name.
211	Set sequence length to value of <211>
212	Replace molecule type (i) 'ADN' with 'DNA', (ii) 'ARN' with 'RNA'
212	Replace molecule type 'PRT' with 'AA'
213	Replace 'Artificial Sequence' and specified equivalents with 'synthetic construct'
213	Replace FR and DE translations of 'Artificial Sequence' and specified equivalents (*'Séquence artificielle', 'Künstliche Sequenz')* with 'synthetic construct'
213	Replace 'Unknown' and specified equivalents with 'unidentified'
213	Replace FR and DE translations of 'Unknown' and specified equivalents (*'inconnu', 'unbekannt')* with 'unidentified'
221	Replace obsolete feature key with recommended key (Scenario 8, ST.26, Annex VII)
221	Replace custom feature key with recommended key (Scenario 12, ST.26, Annex VII)
221	Replace VARSPLIC key with VAR_SEQ (Scenario 13, ST.26, Annex VII)
221	Skip transformation of feature key if 1) molecule type is PRT and 2) feature key is NOT valid ST.26 and 3) the tool can't determine whether the location is a single position or a range of positions
222	Clean feature location value provided (i.e., remove parentheses, replace invalid separator, reduce redundant ranges)
222 (negative value)	If negative numbering in PRT sequence, the feature location need to be corrected (see Scenario 16, ST.26, Annex VII).
222 (missing)	Provide a warning that feature location is missing in import report OR does it provide a feature location of 1..sequence length
223	Import value of 223 after replacing the obsolete feature key with recommended key (Scenario 8, ST.26, Annex VII)
223	Import value of 223 after replacing custom feature key with recommended key (Scenario 12, ST.26, Annex VII).
223	Import 223 after replacing VARSPLIC key with VAR_SEQ (Scenario 13, ST.26, Annex VII).
300-313	Discard publication information provided
400	Replace 'u' with 't' in RNA sequence.
400	Replace 'u' with 't' in DNA sequence.
400	Replace amino acid symbols in 3-letter code with 1-letter code.
400	Provide a warning that the annotation of 'Xaa' symbols must be reviewed in the import report
400	Set skipped indicator to 'yes' for those with a 400 value of '000'
n.a.	Create mandatory source/SOURCE feature for each sequence that: 1) is NOT intentionally skipped and 2) does NOT already have a source feature.
n.a.	Set value of qualifier /mol_type for 'synthetic construct' and protein sequences
n.a.	Notify the user to set the value of qualifier /mol_type.
n.a.	Notify the user to set/review the value of the mandatory qualifier